IN THE CLAIMS

Please replace all prior versions and claims listings with the following claims listing Claims Listing:

1-2. (cancel)

3. (currently amended) ~~A method for detecting aberrant promoter methylation associated with predisposition for cancers of the breast, lung, and colon, in a human comprising detecting methylation of the PAX5 β gene~~ A method of monitoring for cancer in a biological specimen containing DNA from cells suspected of being cancerous and having PAX5 β gene-specific promoter methylation comprising the steps of:

subjecting DNA to bisulfite modification;

expanding the number of copies of at least a portion of the PAX5 β gene by a polymerase chain reaction to amplify the portion of the PAX5 β gene where the promoter methylation resides, thereby generating an amplification product; and

using an aliquot of the amplification product generated by the first polymerase chain reaction in a second, methylation-specific, polymerase chain reaction at a temperature of annealing that exceeds the melting temperature of the second primer set to amplify a portion of the gene's CpG island where the promoter methylation resides and detect the presence of inactivation of the PAX5 β gene.

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4-6. (cancel)

7. (currently amended) A method of monitoring for cancer in a biological specimen containing DNA from cells suspected of being cancerous and having PAX5 α gene-specific promoter methylation ~~human, comprising detecting gene inactivation in a biological fluid by ascertaining the presence of gene-specific promoter methylation in the cells of the biological fluid, and further~~ comprising the steps of:

subjecting DNA ~~in the biological fluid~~ to bisulfite modification;

expanding the number of copies of at least a portion of the PAX5 α gene by using ~~in the DNA by using primer sequences which recognize the bisulfite-modified DNA template, but which not discriminate between methylated and unmethylated alleles, in~~ a polymerase chain reaction to amplify a ~~CpG-rich~~ portion of the PAX5 α gene where the promoter methylation resides, thereby generating an amplification product ~~containing fragments of the PAX5 α gene~~; and

using an aliquot of the amplification product generated by the first polymerase chain reaction in a second, methylation-specific, polymerase chain reaction ~~employing primer sequences specific to a methylated DNA template to~~ at a temperature of annealing that exceeds the melting temperature of the second primer set to amplify a portion of the gene's CpG island where the promoter methylation resides and detect the presence of inactivation of the PAX5 α gene

8-9. (cancel)

10. (new) The method of claim 3 wherein the step of expanding at least a portion of the PAX5 β gene comprises amplifying a 328 base pair fragment with a primer set comprising:

Forward 5' agtttgtgggttgtttagttaatgg

Reverse 5' caaaaaatcccaaccaccaaaacc

11. (new) The method of claim 3 wherein the biological sample from which the DNA is obtained is selected from tissue, plasma, ejaculate, cerebrospinal fluid, serum, mammary duct fluid, urine, fecal stool, and sputum.

12. (new) The method of claim 7 wherein the step of expanding at least a portion of the PAX5 α gene comprises amplifying a 389 base pair fragment with a primer set comprising :

Forward 5' gggtttgtatatggagatgttatagg

Reverse 5' caacatcacaaaatatccccaaacac

13. (new) The method of claim 7 wherein the biological sample from which the DNA is obtained is selected from tissue, plasma, ejaculate, cerebrospinal fluid, serum, mammary duct fluid, urine, fecal stool, and sputum.